

TherapheresisSeq Listing.txt
SEQUENCE LISTING

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<110> Universitaet Stuttgart
      PFIZENMAIER, Klaus
      SCHEURICH, Peter
      GRUNWALD, Ingo
      KRIPPNER-HEIDENREICH, Anja

<120> RECOMBINANT POLYPEPTIDES OF THE MEMBERS OF THE TNF LIGAND FAMILY AND USE
      THEREOF

<130> 040045-0358701

<140> 10/594,189
<141> 2006-09-25

<150> PCT/EP2005/003158
<151> 2005-03-24

<150> DE 102004014983.6-4
<151> 2004-03-26

<160> 41

<170> PatentIn version 3.3

<210> 1
<211> 8
<212> PRT
<213> Artificial Sequence Sequence

<220>
<223> Description of Artificial Sequence: Synthetic flag-tag peptide sequence

<400> 1
Asp Tyr Lys Asp Asp Asp Asp Lys
1          5

<210> 2
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Peptide linker sequence

<400> 2
Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
1          5          10

<210> 3
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Peptide linker sequence

<400> 3

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Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
1 5 10 15

<210> 4
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Linker sequence

<400> 4
ggtaggcgggtt ctggtggcgg ttctggtggc ggatcc 36

<210> 5
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Linker sequence

<400> 5
ggtaggcgggtt ctggtggcgg ttctggtggc ggttctggtg gcggatcc 48

<210> 6
<211> 84
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: sCTNF Primer I

<400> 6
tcgattaagc ttcccggggg atccgccacc agaaccgcca ccagaaccgc caccagagc 60
gatgataccg aagtaaacct gacc 84

<210> 7
<211> 97
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: sCTNF Primer II

<400> 7
atcgattaag cttcccgggg gatccgccac cagaaccgcc accagaaccg ccaccagaac 60
cgccaccag agcgatgata ccgaagtaaa cctgacc 97

<210> 8
<211> 43
<212> DNA
<213> Artificial Sequence

<220>

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<223> Description of Artificial Sequence: sCTNF Primer III

<400> 8
 ccccgaaattc ggatcctctt ctcgtacccc gtctgacaaa ccg 43

<210> 9
 <211> 53
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: sCTNF Primer IV

<400> 9
 gggggggaag cttatcgata gttagatatc atcacagagc gatgataccg aag 53

<210> 10
 <211> 41
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: sCTNF Primer V

<400> 10
 cctgtacctg atctactccc aggttctgtt caaaggccag g 41

<210> 11
 <211> 97
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: cys-sCTNF Primer VI

<400> 11
 aattcattaa agaggagaaa ttaactatgg gagagctcat cgaaggctgc tgcgccggtg 60
 gatctggtca tcatcatcac catcacggct cagacgg 97

<210> 12
 <211> 97
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: cys-sCTNF Primer VII

<400> 12
 cgctccgtct gagccgtgat ggtgatgatg atgaccagat ccaccggcgc agcgaccttc 60
 gatgagctct cccatagtta atttctcctc tttaatg 97

<210> 13
 <211> 100
 <212> DNA
 <213> Artificial Sequence

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<220>
 <223> Description of Artificial Sequence: Primer FasL#1R
 <400> 13
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 cgccaccgag cttatataag ccgaaaaaacg tctgagattc 100
 <210> 14
 <211> 35
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Primer FasL#2F
 <400> 14
 ggggtagcgg ccgcgctgtc gacgattaca aagac 35
 <210> 15
 <211> 26
 <212> DNA
 <213> Artificial Sequence
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 <223> Description of Artificial Sequence: Primer FasL#3F
 <400> 15
 agaaaaaaag gagctgagga aagtgg 26
 <210> 16
 <211> 36
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Primer FasL#4F
 <400> 16
 ggggcggatc cgaaaaaaag gagctgagga aagtgg 36
 <210> 17
 <211> 50
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Primer FasL#5R
 <400> 17
 ggggcctcta gaatcgatgg tcagagctta tataagccga aaaacgtctg 50
 <210> 18
 <211> 51
 <212> DNA
 <213> Artificial Sequence
 <220>

<223> Description of Artificial Sequence: Primer HA-IF
 <400> 18
 cgccatggct atcatctacc tcatacctcct gttcaccgct gtgcggggag c 51

 <210> 19
 <211> 60
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Primer HA-IIR
 <400> 19
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 <210> 20
 <211> 106
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Primer TRAIL#1R
 <400> 20
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 cgccaccgcc aactaaaaag gccccgaaaa aactggcttc atggtc 106

 <210> 21
 <211> 46
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Primer TRAIL#2F
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 <210> 22
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Primer TRAIL#3F
 <400> 22
 aacctctgag gaaaccattt ctacag 26

 <210> 23
 <211> 36
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Primer TRAIL#4F

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<400> 23
ggggcgatc cacctctgag gaaaccattt ctacag 36

<210> 24
<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer TRAIL#5R

<400> 24
ggggcctcta gaatcgatgg tcagccaact aaaaaggccc cgaaaaaact ggc 53

<210> 25
<211> 1506
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: scTNF-L short chain

<220>
<221> CDS
<222> (1)..(1503)

<400> 25
atg aga gga tcg cat cac cat cac cat cac gga tca gcg tcg tct tct 48
Met Arg Gly Ser His His His His His His Gly Ser Ala Ser Ser Ser
1 5 10 15

tct cgt acc ccg tct gac aaa ccg gtt gct cac gtt gtt gca aac ccg 96
Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val Val Ala Asn Pro
20 25 30

cag gct gaa ggt caa ctg caa tgg ctg aac cgt cgt gct aac gct ctg 144
Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu
35 40 45

ctg gct aac ggt gtt gaa ctg cgt gac aac cag ctg gtt gtt ccg tct 192
Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser
50 55 60

gaa ggc ctg tac ctg atc tac tcc cag gtt ctg ttc aaa ggc cag ggc 240
Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly
65 70 75 80

tgc ccg tcc acc cac gtt ctg ctg acc cac acc atc tct cgt atc gct 288
Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala
85 90 95

gtt tcc tac cag acc aaa gta aac ctg ctg tct gca atc aaa tct ccg 336
Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro
100 105 110

tgc cag cgt gaa acc ccg gaa ggt gct gaa gct aaa ccg tgg tac gaa 384
Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu
115 120 125

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ccg atc tac ctg ggt ggc gtt ttt caa ctg gag aaa ggt gac cgt ctg Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu 130 135 140	432
tct gca gaa att aac cgt ccg gac tac ctg gac ttc gca gaa tct ggt Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly 145 150 155 160	480
cag gtt tac ttc ggt atc atc gct ctg ggt ggc ggt tct ggt ggc ggt Gln Val Tyr Phe Gly Ile Ile Ala Leu Gly Gly Gly Ser Gly Gly Gly 165 170 175	528
tct ggt ggc gga tcc tct tct cgt acc ccg tct gac aaa ccg gtt gct Ser Gly Gly Gly Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala 180 185 190	576
cac gtt gtt gca aac ccg cag gct gaa ggt caa ctg caa tgg ctg aac His Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn 195 200 205	624
cgt cgt gct aac gct ctg ctg gct aac ggt gtt gaa ctg cgt gac aac Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn 210 215 220	672
cag ctg gtt gtt ccg tct gaa ggc ctg tac ctg atc tac tcc cag gtt Gln Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val 225 230 235 240	720
ctg ttc aaa ggc cag ggc tgc ccg tcc acc cac gtt ctg ctg acc cac Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His 245 250 255	768
acc atc tct cgt atc gct gtt tcc tac cag acc aaa gta aac ctg ctg Thr Ile Ser Arg Ile Ala Val Ser Tyr 265 Gln Thr Lys Val Asn Leu Leu 260 270	816
tct gca atc aaa tct ccg tgc cag cgt gaa acc ccg gaa ggt gct gaa Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu 275 280 285	864
gct aaa ccg tgg tac gaa ccg atc tac ctg ggt ggc gtt ttt caa ctg Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu 290 295 300	912
gag aaa ggt gac cgt ctg tct gca gaa att aac cgt ccg gac tac ctg Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu 305 310 315 320	960
gac ttc gca gaa tct ggt cag gtt tac ttc ggt atc atc gct ctg ggt Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu Gly 325 330 335	1008
ggc ggt tct ggt ggc ggt tct ggt ggc gga tcc tct tct cgt acc ccg Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser Ser Arg Thr Pro 340 345 350	1056
tct gac aaa ccg gtt gct cac gtt gtt gca aac ccg cag gct gaa ggt Ser Asp Lys Pro Val Ala His Val Val Ala Asn Pro Gln Ala Glu Gly 355 360 365	1104
caa ctg caa tgg ctg aac cgt cgt gct aac gct ctg ctg gct aac ggt Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly 370 375 380	1152

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gtt gaa ctg cgt gac aac cag ctg gtt gtt ccg tct gaa ggc ctg tac 1200
Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser Glu Gly Leu Tyr
385 390 395 400

ctg atc tac tcc cag gtt ctg ttc aaa ggc cag ggc tgc ccg tcc acc 1248
Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr
405 410 415

cac gtt ctg ctg acc cac acc atc tct cgt atc gct gtt tcc tac cag 1296
His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln
420 425 430

acc aaa gta aac ctg ctg tct gca atc aaa tct ccg tgc cag cgt gaa 1344
Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu
435 440 445

acc ccg gaa ggt gct gaa gct aaa ccg tgg tac gaa ccg atc tac ctg 1392
Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu
450 455 460

ggt ggc gtt ttt caa ctg gag aaa ggt gac cgt ctg tct gca gaa att 1440
Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile
465 470 475 480

aac cgt ccg gac tac ctg gac ttc gca gaa tct ggt cag gtt tac ttc 1488
Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe
485 490 495

ggt atc atc gct ctg tga 1506
Gly Ile Ile Ala Leu
500

<210> 26
<211> 501
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: sCTNF-L short chain peptide

<400> 26

Met Arg Gly Ser His His His His His Gly Ser Ala Ser Ser Ser
1 5 10 15

Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val Val Ala Asn Pro
20 25 30

Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu
35 40 45

Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser
50 55 60

Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly
65 70 75 80

TherapheresisSeq Listing.txt

Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala
 85 90 95
 Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro
 100 105 110
 Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu
 115 120 125
 Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu
 130 135 140
 Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly
 145 150 155 160
 Gln Val Tyr Phe Gly Ile Ile Ala Leu Gly Gly Gly Ser Gly Gly Gly
 165 170 175
 Ser Gly Gly Gly Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala
 180 185 190
 His Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn
 195 200 205
 Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn
 210 215 220
 Gln Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val
 225 230 235 240
 Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His
 245 250 255
 Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu
 260 265 270
 Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu
 275 280 285
 Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu
 290 295 300
 Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu
 305 310 315 320
 Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu Gly
 325 330 335

TherapheresisSeq Listing.txt

Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser Ser Arg Thr Pro
340 345 350

Ser Asp Lys Pro Val Ala His Val Val Ala Asn Pro Gln Ala Glu Gly
355 360 365

Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly
370 375 380

Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser Glu Gly Leu Tyr
385 390 395 400

Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr
405 410 415

His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln
420 425 430

Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu
435 440 445

Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu
450 455 460

Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile
465 470 475 480

Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe
485 490 495

Gly Ile Ile Ala Leu
500

<210> 27
<211> 1542
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: cys-sCTNF-L short chain

<220>
<221> CDS
<222> (1)..(1539)

<400> 27
atg gga gag ctc atc gaa ggt cgc tgc gcc ggt gga tct ggt cat cat
Met Gly Glu Leu Ile Glu Gly Arg Cys Ala Gly Gly Ser Gly His His
1 5 10 15

48

TherapheresisSeq Listing.txt

cat cac cat cac ggc tca gac gga gcg tcg tct tct tct cgt acc ccg His His His His Gly Ser Asp Gly Ala Ser Ser Ser Ser Arg Thr Pro 20 25 30	96
tct gac aaa ccg gtt gct cac gtt gtt gca aac ccg cag gct gaa ggt Ser Asp Lys Pro Val Ala His Val Val Ala Asn Pro Gln Ala Glu Gly 35 40 45	144
caa ctg caa tgg ctg aac cgt cgt gct aac gct ctg ctg gct aac ggt Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly 50 55 60	192
gtt gaa ctg cgt gac aac cag ctg gtt gtt ccg tct gaa ggc ctg tac Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser Glu Gly Leu Tyr 65 70 75 80	240
ctg atc tac tcc cag gtt ctg ttc aaa ggc cag ggc tgc ccg tcc acc Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr 85 90 95	288
cac gtt ctg ctg acc cac acc atc tct cgt atc gct gtt tcc tac cag His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln 100 105 110	336
acc aaa gta aac ctg ctg tct gca atc aaa tct ccg tgc cag cgt gaa Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu 115 120 125	384
acc ccg gaa ggt gct gaa gct aaa ccg tgg tac gaa ccg atc tac ctg Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu 130 135 140	432
ggt ggc gtt ttt caa ctg gag aaa ggt gac cgt ctg tct gca gaa att Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile 145 150 155 160	480
aac cgt ccg gac tac ctg gac ttc gca gaa tct ggt cag gtt tac ttc Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe 165 170 175	528
ggt atc atc gct ctg ggt ggc ggt tct ggt ggc ggt tct ggt ggc gga Gly Ile Ile Ala Leu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly 180 185 190	576
tcc tct tct cgt acc ccg tct gac aaa ccg gtt gct cac gtt gtt gca Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val Val Ala 195 200 205	624
aac ccg cag gct gaa ggt caa ctg caa tgg ctg aac cgt cgt gct aac Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn 210 215 220	672
gct ctg ctg gct aac ggt gtt gaa ctg cgt gac aac cag ctg gtt gtt Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val 225 230 235 240	720
ccg tct gaa ggc ctg tac ctg atc tac tcc cag gtt ctg ttc aaa ggc Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly 245 250 255	768
cag ggc tgc ccg tcc acc cac gtt ctg ctg acc cac acc atc tct cgt Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile Ser Arg 260 265 270 275 280 285 290	816

TherapheresisSeq Listing.txt

260	265	270			
atc gct gtt tcc tac cag acc Ile Ala Val Ser Tyr Gln Thr	aaa gta aac ctg ctg tct Lys Val Asn Leu Leu Ser	gca atc aaa Ala Ile Lys	864		
275	280	285			
tct ccg tgc cag cgt gaa acc Ser Pro Cys Gln Arg Glu Thr	ccg gaa ggt gct gaa gct Pro Glu Gly Ala Glu Ala	aaa ccg tgg Lys Pro Trp	912		
290	295	300			
tac gaa ccg atc tac ctg ggt ggc gtt ttt caa ctg gag aaa ggt gac Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp	305	310	315	320	960
cgt ctg tct gca gaa att aac cgt ccg gac tac ctg gac ttc gca gaa Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu	325	330	335	1008	
tct ggt cag gtt tac ttc ggt atc atc gct ctg ggt ggc ggt tct ggt Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu Gly Gly Gly Ser Gly	340	345	350	1056	
ggc ggt tct ggt ggc gga tcc tct tct cgt acc ccg tct gac aaa ccg Gly Gly Ser Gly Gly Gly Ser Ser Arg Thr Pro Ser Asp Lys Pro	355	360	365	1104	
gtt gct cac gtt gtt gca aac ccg cag gct gaa ggt caa ctg caa tgg Val Ala His Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp	370	375	380	1152	
ctg aac cgt cgt gct aac gct ctg ctg gct aac ggt gtt gaa ctg cgt Leu Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg	385	390	395	400	1200
gac aac cag ctg gtt gtt ccg tct gaa ggc ctg tac ctg atc tac tcc Asp Asn Gln Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser	405	410	415	1248	
cag gtt ctg ttc aaa ggc cag ggc tgc ccg tcc acc cac gtt ctg ctg Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu	420	425	430	1296	
acc cac acc atc tct cgt atc gct gtt tcc tac cag acc aaa gta aac Thr His Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn	435	440	445	1344	
ctg ctg tct gca atc aaa tct ccg tgc cag cgt gaa acc ccg gaa ggt Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly	450	455	460	1392	
gct gaa gct aaa ccg tgg tac gaa ccg atc tac ctg ggt ggc gtt ttt Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe	465	470	475	480	1440
caa ctg gag aaa ggt gac cgt ctg tct gca gaa att aac cgt ccg gac Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp	485	490	495	1488	
tac ctg gac ttc gca gaa tct ggt cag gtt tac ttc ggt atc atc gct Tyr Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala	500	505	510	1536	
ctg tga			1542		

TherapheresisSeq Listing.txt

Leu

<210> 28
 <211> 513
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: cys-sCTNF-L short peptide
 <400> 28

Met Gly Glu Leu Ile Glu Gly Arg Cys Ala Gly Gly Ser Gly His His
 1 5 10 15

His His His His Gly Ser Asp Gly Ala Ser Ser Ser Ser Arg Thr Pro
 20 25 30

Ser Asp Lys Pro Val Ala His Val Val Ala Asn Pro Gln Ala Glu Gly
 35 40 45

Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly
 50 55 60

Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser Glu Gly Leu Tyr
 65 70 75 80

Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr
 85 90 95

His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln
 100 105 110

Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu
 115 120 125

Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu
 130 135 140

Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile
 145 150 155 160

Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe
 165 170 175

Gly Ile Ile Ala Leu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly
 180 185 190

Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val Val Ala

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195

200

205

Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn
210 215 220

Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val
225 230 235 240

Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly
245 250 255

Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile Ser Arg
260 265 270

Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys
275 280 285

Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp
290 295 300

Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp
305 310 315 320

Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu
325 330 335

Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu Gly Gly Gly Ser Gly
340 345 350

Gly Gly Ser Gly Gly Gly Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro
355 360 365

Val Ala His Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp
370 375 380

Leu Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg
385 390 395 400

Asp Asn Gln Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser
405 410 415

Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu
420 425 430

Thr His Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn
435 440 445

TherapheresisSeq Listing.txt

Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly
450 455 460

Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe
465 470 475 480

Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp
485 490 495

Tyr Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala
500 505 510

Leu

<210> 29
<211> 1476
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: scFasL sequence

<220>
<221> CDS
<222> (1)..(1473)

<400> 29	
atg gct atc atc tac ctc atc ctc ctg ttc acc gct gtg cgg ggc gcg	48
Met Ala Ile Ile Tyr Leu Ile Leu Leu Phe Thr Ala Val Arg Gly Ala	
1 5 10 15	
gcc gcg gat tac aaa gac gat gac gat aaa gaa ttc acg cgt gaa aaa	96
Ala Ala Asp Tyr Lys Asp Asp Asp Asp Lys Glu Phe Thr Arg Glu Lys	
20 25 30	
aag gag ctg agg aaa gtg gcc cat tta aca ggc aag tcc aac tca agg	144
Lys Glu Leu Arg Lys Val Ala His Leu Thr Gly Lys Ser Asn Ser Arg	
35 40 45	
tcc atg cct ctg gaa tgg gaa gac acc tat gga att gtc ctg ctt tct	192
Ser Met Pro Leu Glu Trp Glu Asp Thr Tyr Gly Ile Val Leu Leu Ser	
50 55 60	
gga gtg aag tat aag aag ggt ggc ctt gtg atc aat gaa act ggg ctg	240
Gly Val Lys Tyr Lys Lys Gly Gly Leu Val Ile Asn Glu Thr Gly Leu	
65 70 75 80	
tac ttt gta tat tcc aaa gta tac ttc cgg ggt caa tct tgc aac aac	288
Tyr Phe Val Tyr Ser Lys Val Tyr Phe Arg Gly Gln Ser Cys Asn Asn	
85 90 95	
ctg ccc ctg agc cac aag gtc tac atg agg aac tct aag tat ccc cag	336
Leu Pro Leu Ser His Lys Val Tyr Met Arg Asn Ser Lys Tyr Pro Gln	
100 105 110	
gat ctg gtg atg atg gag ggg aag atg atg agc tac tgc act act ggg	384

TherapheresisSeq Listing.txt

Asp	Leu	Val	Met	Met	Glu	Gly	Lys	Met	Met	Ser	Tyr	Cys	Thr	Thr	Gly	
		115					120					125				
cag	atg	tgg	gcc	cgc	agc	agc	tac	ctg	ggg	gca	gtg	ttc	aat	ctt	acc	432
Gln	Met	Trp	Ala	Arg	Ser	Ser	Tyr	Leu	Gly	Ala	Val	Phe	Asn	Leu	Thr	
		130				135					140					
agt	gct	gat	cat	tta	tat	gtc	aac	gta	tct	gag	ctc	tct	ctg	gtc	aat	480
Ser	Ala	Asp	His	Leu	Tyr	Val	Asn	Val	Ser	Glu	Leu	Ser	Leu	Val	Asn	
		145			150					155					160	
ttt	gag	gaa	tct	cag	acg	ttt	ttc	ggc	tta	tat	aag	ctc	ggt	ggc	ggt	528
Phe	Glu	Glu	Ser	Gln	Thr	Phe	Phe	Gly	Leu	Tyr	Lys	Leu	Gly	Gly	Gly	
				165					170					175		
tct	ggt	ggc	ggt	tct	ggt	ggc	ggt	tct	ggt	ggc	gga	tca	gaa	aaa	aag	576
Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Glu	Lys	Lys	
			180					185					190			
gag	ctg	agg	aaa	gtg	gcc	cat	tta	aca	ggc	aag	tcc	aac	tca	agg	tcc	624
Glu	Leu	Arg	Lys	Val	Ala	His	Leu	Thr	Gly	Lys	Ser	Asn	Ser	Arg	Ser	
		195					200					205				
atg	cct	ctg	gaa	tgg	gaa	gac	acc	tat	gga	att	gtc	ctg	ctt	tct	gga	672
Met	Pro	Leu	Glu	Trp	Glu	Asp	Thr	Tyr	Gly	Ile	Val	Leu	Leu	Ser	Gly	
		210				215					220					
gtg	aag	tat	aag	aag	ggt	ggc	ctt	gtg	atc	aat	gaa	act	ggg	ctg	tac	720
Val	Lys	Tyr	Lys	Lys	Gly	Gly	Leu	Val	Ile	Asn	Glu	Thr	Gly	Leu	Tyr	
		225			230					235				240		
ttt	gta	tat	tcc	aaa	gta	tac	ttc	cgg	ggt	caa	tct	tgc	aac	aac	ctg	768
Phe	Val	Tyr	Ser	Lys	Val	Tyr	Phe	Arg	Gly	Gln	Ser	Cys	Asn	Asn	Leu	
				245					250					255		
ccc	ctg	agc	cac	aag	gtc	tac	atg	agg	aac	tct	aag	tat	ccc	cag	gat	816
Pro	Leu	Ser	His	Lys	Val	Tyr	Met	Arg	Asn	Ser	Lys	Tyr	Pro	Gln	Asp	
			260					265					270			
ctg	gtg	atg	atg	gag	ggg	aag	atg	atg	agc	tac	tgc	act	act	ggg	cag	864
Leu	Val	Met	Met	Glu	Gly	Lys	Met	Met	Ser	Tyr	Cys	Thr	Thr	Gly	Gln	
		275					280					285				
atg	tgg	gcc	cgc	agc	agc	tac	ctg	ggg	gca	gtg	ttc	aat	ctt	acc	agt	912
Met	Trp	Ala	Arg	Ser	Ser	Tyr	Leu	Gly	Ala	Val	Phe	Asn	Leu	Thr	Ser	
		290				295					300					
gct	gat	cat	tta	tat	gtc	aac	gta	tct	gag	ctc	tct	ctg	gtc	aat	ttt	960
Ala	Asp	His	Leu	Tyr	Val	Asn	Val	Ser	Glu	Leu	Ser	Leu	Val	Asn	Phe	
		305			310					315					320	
gag	gaa	tct	cag	acg	ttt	ttc	ggc	tta	tat	aag	ctc	ggt	ggc	ggt	tct	1008
Glu	Glu	Ser	Gln	Thr	Phe	Phe	Gly	Leu	Tyr	Lys	Leu	Gly	Gly	Gly	Ser	
				325					330					335		
ggt	ggc	ggt	tct	ggt	ggc	ggt	tct	ggt	ggc	gga	tcc	gaa	aaa	aag	gag	1056
Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Glu	Lys	Lys	Glu	
			340				345					350				
ctg	agg	aaa	gtg	gcc	cat	tta	aca	ggc	aag	tcc	aac	tca	agg	tcc	atg	1104
Leu	Arg	Lys	Val	Ala	His	Leu	Thr	Gly	Lys	Ser	Asn	Ser	Arg	Ser	Met	
		355					360					365				

TherapheresisSeq Listing.txt

cct ctg gaa tgg gaa gac acc tat gga att gtc ctg ctt tct gga gtg 1152
Pro Leu Glu Trp Glu Asp Thr Tyr Gly Ile Val Leu Leu Ser Gly Val
370 375 380

aag tat aag aag ggt ggc ctt gtg atc aat gaa act ggg ctg tac ttt 1200
Lys Tyr Lys Lys Gly Gly Leu Val Ile Asn Glu Thr Gly Leu Tyr Phe
385 390 395 400

gta tat tcc aaa gta tac ttc cgg ggt caa tct tgc aac aac ctg ccc 1248
Val Tyr Ser Lys Val Tyr Phe Arg Gly Gln Ser Cys Asn Asn Leu Pro
405 410 415

ctg agc cac aag gtc tac atg agg aac tct aag tat ccc cag gat ctg 1296
Leu Ser His Lys Val Tyr Met Arg Asn Ser Lys Tyr Pro Gln Asp Leu
420 425 430

gtg atg atg gag ggg aag atg atg agc tac tgc act act ggg cag atg 1344
Val Met Met Glu Gly Lys Met Met Ser Tyr Cys Thr Thr Gly Gln Met
435 440 445

tgg gcc cgc agc agc tac ctg ggg gca gtg ttc aat ctt acc agt gct 1392
Trp Ala Arg Ser Ser Tyr Leu Gly Ala Val Phe Asn Leu Thr Ser Ala
450 455 460

gat cat tta tat gtc aac gta tct gag ctc tct ctg gtc aat ttt gag 1440
Asp His Leu Tyr Val Asn Val Ser Glu Leu Ser Leu Val Asn Phe Glu
465 470 475 480

gaa tct cag acg ttt ttc ggc tta tat aag ctc tga 1476
Glu Ser Gln Thr Phe Phe Gly Leu Tyr Lys Leu
485 490

<210> 30

<211> 491

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: scFasL peptide sequence

<400> 30

Met Ala Ile Ile Tyr Leu Ile Leu Leu Phe Thr Ala Val Arg Gly Ala
1 5 10 15

Ala Ala Asp Tyr Lys Asp Asp Asp Asp Lys Glu Phe Thr Arg Glu Lys
20 25 30

Lys Glu Leu Arg Lys Val Ala His Leu Thr Gly Lys Ser Asn Ser Arg
35 40 45

Ser Met Pro Leu Glu Trp Glu Asp Thr Tyr Gly Ile Val Leu Leu Ser
50 55 60

Gly Val Lys Tyr Lys Lys Gly Gly Leu Val Ile Asn Glu Thr Gly Leu
65 70 75 80

TherapheresisSeq Listing.txt

Tyr Phe Val Tyr Ser Lys Val Tyr Phe Arg Gly Gln Ser Cys Asn Asn
 85 90 95
 Leu Pro Leu Ser His Lys Val Tyr Met Arg Asn Ser Lys Tyr Pro Gln
 100 105 110
 Asp Leu Val Met Met Glu Gly Lys Met Met Ser Tyr Cys Thr Thr Gly
 115 120 125
 Gln Met Trp Ala Arg Ser Ser Tyr Leu Gly Ala Val Phe Asn Leu Thr
 130 135 140
 Ser Ala Asp His Leu Tyr Val Asn Val Ser Glu Leu Ser Leu Val Asn
 145 150 155 160
 Phe Glu Glu Ser Gln Thr Phe Phe Gly Leu Tyr Lys Leu Gly Gly Gly
 165 170 175
 Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu Lys Lys
 180 185 190
 Glu Leu Arg Lys Val Ala His Leu Thr Gly Lys Ser Asn Ser Arg Ser
 195 200 205
 Met Pro Leu Glu Trp Glu Asp Thr Tyr Gly Ile Val Leu Leu Ser Gly
 210 215 220
 Val Lys Tyr Lys Lys Gly Gly Leu Val Ile Asn Glu Thr Gly Leu Tyr
 225 230 235 240
 Phe Val Tyr Ser Lys Val Tyr Phe Arg Gly Gln Ser Cys Asn Asn Leu
 245 250 255
 Pro Leu Ser His Lys Val Tyr Met Arg Asn Ser Lys Tyr Pro Gln Asp
 260 265 270
 Leu Val Met Met Glu Gly Lys Met Met Ser Tyr Cys Thr Thr Gly Gln
 275 280 285
 Met Trp Ala Arg Ser Ser Tyr Leu Gly Ala Val Phe Asn Leu Thr Ser
 290 295 300
 Ala Asp His Leu Tyr Val Asn Val Ser Glu Leu Ser Leu Val Asn Phe
 305 310 315 320
 Glu Glu Ser Gln Thr Phe Phe Gly Leu Tyr Lys Leu Gly Gly Gly Ser
 325 330 335

TherapheresisSeq Listing.txt

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu Lys Lys Glu
340 345 350

Leu Arg Lys Val Ala His Leu Thr Gly Lys Ser Asn Ser Arg Ser Met
355 360 365

Pro Leu Glu Trp Glu Asp Thr Tyr Gly Ile Val Leu Leu Ser Gly Val
370 375 380

Lys Tyr Lys Lys Gly Gly Leu Val Ile Asn Glu Thr Gly Leu Tyr Phe
385 390 395 400

Val Tyr Ser Lys Val Tyr Phe Arg Gly Gln Ser Cys Asn Asn Leu Pro
405 410 415

Leu Ser His Lys Val Tyr Met Arg Asn Ser Lys Tyr Pro Gln Asp Leu
420 425 430

Val Met Met Glu Gly Lys Met Met Ser Tyr Cys Thr Thr Gly Gln Met
435 440 445

Trp Ala Arg Ser Ser Tyr Leu Gly Ala Val Phe Asn Leu Thr Ser Ala
450 455 460

Asp His Leu Tyr Val Asn Val Ser Glu Leu Ser Leu Val Asn Phe Glu
465 470 475 480

Glu Ser Gln Thr Phe Phe Gly Leu Tyr Lys Leu
485 490

<210> 31
<211> 1869
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: scTRAIL sequence

<220>
<221> CDS
<222> (1)..(1866)

<400> 31	
atg gct atc atc tac ctc atc ctc ctg ttc acc gct gtg cgg ggc gcg	48
Met Ala Ile Ile Tyr Leu Ile Leu Leu Phe Thr Ala Val Arg Gly Ala	
1 5 10 15	

gcc gcg gat tac aaa gac gat gac gat aaa gaa ttc gga acc tct gag	96
Ala Ala Asp Tyr Lys Asp Asp Asp Asp Lys Glu Phe Gly Thr Ser Glu	
20 25 30	

gaa acc att tct aca gtt caa gaa aag caa caa aat att tct ccc cta	144
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TherapheresisSeq Listing.txt

Glu	Thr	Ile	Ser	Thr	Val	Gln	Glu	Lys	Gln	Gln	Asn	Ile	Ser	Pro	Leu	
35							40					45				
gtg	aga	gaa	aga	ggt	cct	cag	aga	gta	gca	gct	cac	ata	act	ggg	acc	192
Val	Arg	Glu	Arg	Gly	Pro	Gln	Arg	Val	Ala	Ala	His	Ile	Thr	Gly	Thr	
50						55					60					
aga	gga	aga	agc	aac	aca	ttg	tct	tct	cca	aac	tcc	aag	aat	gaa	aag	240
Arg	Gly	Arg	Ser	Asn	Thr	Leu	Ser	Ser	Pro	Asn	Ser	Lys	Asn	Glu	Lys	
65					70					75				80		
gct	ctg	ggc	cgc	aaa	ata	aac	tcc	tgg	gaa	tca	tca	agg	agt	ggg	cat	288
Ala	Leu	Gly	Arg	Lys	Ile	Asn	Ser	Trp	Glu	Ser	Ser	Arg	Ser	Gly	His	
				85					90					95		
tca	ttc	ctg	agc	aac	ttg	cac	ttg	agg	aat	ggt	gaa	ctg	gtc	atc	cat	336
Ser	Phe	Leu		Asn	Leu	His	Leu	Arg	Asn	Gly	Glu	Leu	Val	Ile	His	
			100				105					110				
gaa	aaa	ggg	ttt	tac	tac	atc	tat	tcc	caa	aca	tac	ttt	cga	ttt	cag	384
Glu	Lys	Gly	Phe	Tyr	Tyr	Ile	Tyr	Ser	Gln	Thr	Tyr	Phe	Arg	Phe	Gln	
		115					120					125				
gag	gaa	ata	aaa	gaa	aac	aca	aag	aac	gac	aaa	caa	atg	gtc	caa	tat	432
Glu	Glu	Ile	Lys	Glu	Asn	Thr	Lys	Asn	Asp	Lys	Gln	Met	Val	Gln	Tyr	
	130					135					140					
att	tac	aaa	tac	aca	agt	tat	cct	gac	cct	ata	ttg	ttg	atg	aaa	agt	480
Ile	Tyr	Lys	Tyr	Thr	Ser	Tyr	Pro	Asp	Pro	Ile	Leu	Leu	Met	Lys	Ser	
145					150					155					160	
gct	aga	aat	agt	tgt	tgg	tct	aaa	gat	gca	gaa	tat	gga	ctc	tat	tcc	528
Ala	Arg	Asn	Ser	Cys	Trp	Ser	Lys	Asp	Ala	Glu	Tyr	Gly	Leu	Tyr	Ser	
				165					170					175		
atc	tat	caa	ggg	gga	ata	ttt	gag	ctt	aag	gaa	aat	gac	aga	att	ttt	576
Ile	Tyr	Gln	Gly	Gly	Ile	Phe	Glu	Leu	Lys	Glu	Asn	Asp	Arg	Ile	Phe	
			180				185						190			
gtt	tct	gta	aca	aat	gag	cac	ttg	ata	gac	atg	gac	cat	gaa	gcc	agt	624
Val	Ser	Val	Thr	Asn	Glu	His	Leu	Ile	Asp	Met	Asp	His	Glu	Ala	Ser	
		195					200					205				
ttt	ttc	ggg	gcc	ttt	tta	gtt	ggc	ggt	ggc	ggt	tct	ggt	ggc	ggt	tct	672
Phe	Phe	Gly	Ala	Phe	Leu	Val	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	
	210					215					220					
ggt	ggc	ggt	tct	ggt	ggc	gga	tca	acc	tct	gag	gaa	acc	att	tct	aca	720
Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Thr	Ser	Glu	Glu	Thr	Ile	Ser	Thr	
225					230					235					240	
gtt	caa	gaa	aag	caa	caa	aat	att	tct	ccc	cta	gtg	aga	gaa	aga	ggt	768
Val	Gln	Glu	Lys	Gln	Gln	Asn	Ile	Ser	Pro	Leu	Val	Arg	Glu	Arg	Gly	
				245					250					255		
cct	cag	aga	gta	gca	gct	cac	ata	act	ggg	acc	aga	gga	aga	agc	aac	816
Pro	Gln	Arg	Val	Ala	Ala	His	Ile	Thr	Gly	Thr	Arg	Gly	Arg	Ser	Asn	
			260				265					270				
aca	ttg	tct	tct	cca	aac	tcc	aag	aat	gaa	aag	gct	ctg	ggc	cgc	aaa	864
Thr	Leu	Ser	Ser	Pro	Asn	Ser	Lys	Asn	Glu	Lys	Ala	Leu	Gly	Arg	Lys	
		275					280					285				

TherapheresisSeq Listing.txt

ata Ile	aac Asn	tcc Ser	tgg Trp	gaa Glu	tca Ser	tca Ser	agg Arg	agt Ser	ggg Gly	cat His	tca Ser	ttc Phe	ctg Leu	agc Ser	aac Asn	912
290						295					300					
ttg Leu	cac His	ttg Leu	agg Arg	aat Asn	ggg Gly	gaa Glu	ctg Leu	gtc Val	atc Ile	cat His	gaa Glu	aaa Lys	ggg Gly	ttt Phe	tac Tyr	960
305					310					315					320	
tac Tyr	atc Ile	tat Tyr	tcc Ser	caa Gln	aca Thr	tac Tyr	ttt Phe	cga Arg	ttt Phe	cag Gln	gag Glu	gaa Glu	ata Ile	aaa Lys	gaa Glu	1008
				325					330					335		
aac Asn	aca Thr	aag Lys	aac Asn	gac Asp	aaa Lys	caa Gln	atg Met	gtc Val	caa Gln	tat Tyr	att Ile	tac Tyr	aaa Lys	tac Tyr	aca Thr	1056
				340				345					350			
agt Ser	tat Tyr	cct Pro	gac Asp	cct Pro	ata Ile	ttg Leu	ttg Leu	atg Met	aaa Lys	agt Ser	gct Ala	aga Arg	aat Asn	agt Ser	tgt Cys	1104
		355					360					365				
tgg Trp	tct Ser	aaa Lys	gat Asp	gca Ala	gaa Glu	tat Tyr	gga Gly	ctc Leu	tat Tyr	tcc Ser	atc Ile	tat Tyr	caa Gln	ggg Gly	gga Gly	1152
		370				375					380					
ata Ile	ttt Phe	gag Glu	ctt Leu	aag Lys	gaa Glu	aat Asn	gac Asp	aga Arg	att Ile	ttt Phe	gtt Val	tct Ser	gta Val	aca Thr	aat Asn	1200
385					390					395					400	
gag Glu	cac His	ttg Leu	ata Ile	gac Asp	atg Met	gac Asp	cat His	gaa Glu	gcc Ala	agt Ser	ttt Phe	ttc Phe	ggg Gly	gcc Ala	ttt Phe	1248
				405					410					415		
tta Leu	gtt Val	ggc Gly	ggg Gly	ggc Gly	ggg Gly	tct Ser	ggg Gly	ggc Gly	ggg Gly	tct Ser	ggg Gly	ggc Gly	ggg Gly	tct Ser	ggg Gly	1296
			420				425						430			
ggc Gly	gga Gly	tcc Ser	acc Thr	tct Ser	gag Glu	gaa Glu	acc Thr	att Ile	tct Ser	aca Thr	gtt Val	caa Gln	gaa Glu	aag Lys	caa Gln	1344
		435					440					445				
caa Gln	aat Asn	att Ile	tct Ser	ccc Pro	cta Leu	gtg Val	aga Arg	gaa Glu	aga Arg	ggg Gly	cct Pro	cag Gln	aga Arg	gta Val	gca Ala	1392
	450					455					460					
gct Ala	cac His	ata Ile	act Thr	ggg Gly	acc Thr	aga Arg	gga Gly	aga Arg	agc Ser	aac Asn	aca Thr	ttg Leu	tct Ser	tct Ser	cca Pro	1440
465				470						475					480	
aac Asn	tcc Ser	aag Lys	aat Asn	gaa Glu	aag Lys	gct Ala	ctg Leu	ggc Gly	cgc Arg	aaa Lys	ata Ile	aac Asn	tcc Ser	tgg Trp	gaa Glu	1488
				485					490					495		
tca Ser	tca Ser	agg Arg	agt Ser	ggg Gly	cat His	tca Ser	ttc Phe	ctg Leu	agc Ser	aac Asn	ttg Leu	cac His	ttg Leu	agg Arg	aat Asn	1536
			500					505					510			
ggg Gly	gaa Glu	ctg Leu	gtc Val	atc Ile	cat His	gaa Glu	aaa Lys	ggg Gly	ttt Phe	tac Tyr	tac Tyr	atc Ile	tat Tyr	tcc Ser	caa Gln	1584
		515					520					525				
aca Thr	tac Tyr	ttt Phe	cga Arg	ttt Phe	cag Gln	gag Glu	gaa Glu	ata Ile	aaa Lys	gaa Glu	aac Asn	aca Thr	aag Lys	aac Asn	gac Asp	1632
	530					535					540					

TherapheresisSeq Listing.txt

aaa caa atg gtc caa tat att tac aaa tac aca agt tat cct gac cct 1680
Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro
545 550 555 560

ata ttg ttg atg aaa agt gct aga aat agt tgt tgg tct aaa gat gca 1728
Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala
565 570 575

gaa tat gga ctc tat tcc atc tat caa ggg gga ata ttt gag ctt aag 1776
Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys
580 585 590

gaa aat gac aga att ttt gtt tct gta aca aat gag cac ttg ata gac 1824
Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His Leu Ile Asp
595 600 605

atg gac cat gaa gcc agt ttt ttc ggg gcc ttt tta gtt ggc tga 1869
Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly
610 615 620

<210> 32
<211> 622
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: scTRAIL peptide sequence

<400> 32

Met Ala Ile Ile Tyr Leu Ile Leu Leu Phe Thr Ala Val Arg Gly Ala
1 5 10 15

Ala Ala Asp Tyr Lys Asp Asp Asp Asp Lys Glu Phe Gly Thr Ser Glu
20 25 30

Glu Thr Ile Ser Thr Val Gln Glu Lys Gln Gln Asn Ile Ser Pro Leu
35 40 45

Val Arg Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr Gly Thr
50 55 60

Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys
65 70 75 80

Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His
85 90 95

Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile His
100 105 110

Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln
115 120 125

TherapheresisSeq Listing.txt

Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr
 130 135 140
 Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser
 145 150 155 160
 Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser
 165 170 175
 Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe
 180 185 190
 Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala Ser
 195 200 205
 Phe Phe Gly Ala Phe Leu Val Gly Gly Gly Gly Ser Gly Gly Gly Ser
 210 215 220
 Gly Gly Gly Ser Gly Gly Gly Ser Thr Ser Glu Glu Thr Ile Ser Thr
 225 230 235 240
 Val Gln Glu Lys Gln Gln Asn Ile Ser Pro Leu Val Arg Glu Arg Gly
 245 250 255
 Pro Gln Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn
 260 265 270
 Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys
 275 280 285
 Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn
 290 295 300
 Leu His Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr
 305 310 315 320
 Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu
 325 330 335
 Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr
 340 345 350
 Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys
 355 360 365
 Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly
 370 375 380

TherapheresisSeq Listing.txt

Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn
385 390 395 400

Glu His Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe
405 410 415

Leu Val Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
420 425 430

Gly Gly Ser Thr Ser Glu Glu Thr Ile Ser Thr Val Gln Glu Lys Gln
435 440 445

Gln Asn Ile Ser Pro Leu Val Arg Glu Arg Gly Pro Gln Arg Val Ala
450 455 460

Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro
465 470 475 480

Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu
485 490 495

Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn
500 505 510

Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln
515 520 525

Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp
530 535 540

Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro
545 550 555 560

Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala
565 570 575

Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys
580 585 590

Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His Leu Ile Asp
595 600 605

Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly
610 615 620

TherapheresisSeq Listing.txt

<211> 1581
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: sCTNF sequence

<220>
<221> CDS
<222> (1)..(1578)

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<400> 33
atg gct atc atc tac ctc atc ctc ctg ttc acc gct gtg cgg ggc gcg      48
Met Ala Ile Ile Tyr Leu Ile Leu Leu Phe Thr Ala Val Arg Gly Ala
1      5      10
gcc gcg gat tac aaa gac gat gac gat aaa gaa ttc gga tca tct tct      96
Ala Ala Asp Tyr Lys Asp Asp Asp Asp Lys Glu Phe Gly Ser Ser Ser
      20      25      30
cga acc ccg agt gac aag cct gta gcc cat gtt gta gca aac cct caa      144
Arg Thr Pro Ser Asp Lys Pro Val Ala His Val Val Ala Asn Pro Gln
      35      40      45
gct gag ggg cag ctc cag tgg ctg aac cgc cgg gcc aat gcc ctc ctg      192
Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu
      50      55      60
gcc aat ggc gtg gag ctg aga gat aac cag ctg gtg gtg cca tca gag      240
Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser Glu
      65      70      75
ggc ctg tac ctc atc tac tcc cag gtc ctc ttc aag ggc caa ggc tgc      288
Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly Cys
      85      90      95
ccc tcc acc cat gtg ctc ctc acc cac acc atc agc cgc atc gcc gtc      336
Pro Ser Thr His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala Val
      100      105      110
tcc tac cag acc aag gtc aac ctc ctc tct gcc atc aag agc ccc tgc      384
Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys
      115      120      125
cag agg gag acc cca gag ggg gct gag gcc aag ccc tgg tat gag ccc      432
Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro
      130      135      140
atc tat ctg gga ggg gtc ttc cag ctg gag aag ggt gac cga ctc agc      480
Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser
      145      150      155
gct gag atc aat cgg ccc gac tat ctc gac ttt gcc gag tct ggg cag      528
Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly Gln
      165      170      175
gtc tac ttt ggg atc att gcc ctg ggt ggc ggt tct ggt ggc ggt tct      576
Val Tyr Phe Gly Ile Ile Ala Leu Gly Gly Gly Ser Gly Gly Gly Ser
      180      185      190
ggt ggc ggt tct ggt ggc gga tca tca tct tct cga acc ccg agt gac      624
Gly Gly Gly Ser Gly Gly Gly Ser Ser Ser Ser Arg Thr Pro Ser Asp

```

TherapheresisSeq Listing.txt

195	200	205	
aag cct gta gcc cat gtt gta gca aac cct caa gct gag ggg cag ctc Lys Pro Val Ala His Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu 210 215 220			672
cag tgg ctg aac cgc cgg gcc aat gcc ctc ctg gcc aat ggc gtg gag Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu 225 230 235 240			720
ctg aga gat aac cag ctg gtg gtg cca tca gag ggc ctg tac ctc atc Leu Arg Asp Asn Gln Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile 245 250 255			768
tac tcc cag gtc ctc ttc aag ggc caa ggc tgc ccc tcc acc cat gtg Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val 260 265 270			816
ctc ctc acc cac acc atc agc cgc atc gcc gtc tcc tac cag acc aag Leu Leu Thr His Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys 275 280 285			864
gtc aac ctc ctc tct gcc atc aag agc ccc tgc cag agg gag acc cca Val Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro 290 295 300			912
gag ggg gct gag gcc aag ccc tgg tat gag ccc atc tat ctg gga ggg Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly 305 310 315 320			960
gtc ttc cag ctg gag aag ggt gac cga ctc agc gct gag atc aat cgg Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg 325 330 335			1008
ccc gac tat ctc gac ttt gcc gag tct ggg cag gtc tac ttt ggg atc Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile 340 345 350			1056
att gcc ctg ggt ggc ggt tct ggt ggc ggt tct ggt ggc ggt tct ggt Ile Ala Leu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly 355 360 365			1104
ggc gga tca tca tct tct cga acc ccg agt gac aag cct gta gcc cat Gly Gly Ser Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His 370 375 380			1152
gtt gta gca aac cct caa gct gag ggg cag ctc cag tgg ctg aac cgc Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg 385 390 395 400			1200
cgg gcc aat gcc ctc ctg gcc aat ggc gtg gag ctg aga gat aac cag Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln 405 410 415			1248
ctg gtg gtg cca tca gag ggc ctg tac ctc atc tac tcc cag gtc ctc Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu 420 425 430			1296
ttc aag ggc caa ggc tgc ccc tcc acc cat gtg ctc ctc acc cac acc Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr 435 440 445			1344
atc agc cgc atc gcc gtc tcc tac cag acc aag gtc aac ctc ctc tct			1392

TherapheresisSeq Listing.txt

Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser
450 455 460

gcc atc aag agc ccc tgc cag agg gag acc cca gag ggg gct gag gcc 1440
Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala
465 470 475 480

aag ccc tgg tat gag ccc atc tat ctg gga ggg gtc ttc cag ctg gag 1488
Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu
485 490 495

aag ggt gac cga ctc agc gct gag atc aat cgg ccc gac tat ctc gac 1536
Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp
500 505 510

ttt gcc gag tct ggg cag gtc tac ttt ggg atc att gcc ctg tga 1581
Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
515 520 525

<210> 34
<211> 526
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: sCTNF peptide sequence
<400> 34

Met Ala Ile Ile Tyr Leu Ile Leu Leu Phe Thr Ala Val Arg Gly Ala
1 5 10 15

Ala Ala Asp Tyr Lys Asp Asp Asp Asp Lys Glu Phe Gly Ser Ser Ser
20 25 30

Arg Thr Pro Ser Asp Lys Pro Val Ala His Val Val Ala Asn Pro Gln
35 40 45

Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu
50 55 60

Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser Glu
65 70 75 80

Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly Cys
85 90 95

Pro Ser Thr His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala Val
100 105 110

Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys
115 120 125

Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro
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TherapheresisSeq_Listing.txt

130

135

140

Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser
145 150 155 160

Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly Gln
165 170 175

Val Tyr Phe Gly Ile Ile Ala Leu Gly Gly Gly Ser Gly Gly Gly Ser
180 185 190

Gly Gly Gly Ser Gly Gly Gly Ser Ser Ser Ser Arg Thr Pro Ser Asp
195 200 205

Lys Pro Val Ala His Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu
210 215 220

Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu
225 230 235 240

Leu Arg Asp Asn Gln Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile
245 250 255

Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val
260 265 270

Leu Leu Thr His Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys
275 280 285

Val Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro
290 295 300

Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly
305 310 315 320

Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg
325 330 335

Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile
340 345 350

Ile Ala Leu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
355 360 365

Gly Gly Ser Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His
370 375 380

Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg
385 390 395 400

Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln
405 410 415

Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu
420 425 430

Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr
435 440 445

Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser
450 455 460

Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala
465 470 475 480

Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu
485 490 495

Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp
500 505 510

Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
515 520 525

<210>	35
<211>	2253
<212>	DNA
<213>	Artificial Sequence

<220>
<223> Description of Artificial Sequence: scFasL-AMAIZE sequence

```
<220>
<221> CDS
<222> (1)..(2250)
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<400> 35
atg gac tgg acc tgg cgc gtg ttt tgc ctg ctc gcc gtg gct cct ggg 48
Met Asp Trp Thr Trp Arg Val Phe Cys Leu Leu Ala Val Ala Pro Gly
1 5 10 15

gcc cac agc cag gta cag ctg gtg cag tct ggg gga ggc atg gta gag 96
Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Gly Gly Met Val Glu
20 25 30

cct ggg ggg tcc ctt aga ctc tcc tgt gca gcc tct gga ttc act ttc 144
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35 40 45

agt aat gcc tgg atg agc tgg gtc cgc cag gct cca ggg aag ggg ctg 192
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TherapheresisSeq Listing.txt

Ser	Asn	Ala	Trp	Met	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	
50					55						60					
gag Glu 65	tgg Trp	gtt Val	ggc Gly	cgt Arg	ata Ile 70	aaa Lys	agc Ser	aaa Lys	gct Ala 75	ggt Gly	ggt Gly	ggg Gly	aca Thr	gca Ala	gag Glu 80	240
tac Tyr	gct Ala	gca Ala	ccc Pro	gtg Val 85	aaa Lys	ggc Gly	aga Arg	ttc Phe	acc Thr 90	atc Ile	tca Ser	aga Arg	gat Asp	gat Asp 95	tca Ser	288
caa Gln	aac Asn	acg Thr	ctg Leu 100	tat Tyr	ctg Leu	caa Gln	atg Met	aac Asn 105	agc Ser	ctg Leu	aaa Lys	acc Thr	gac Asp 110	gac Asp	aca Thr	336
gcc Ala	gtg Val	tat Tyr 115	tac Tyr	tgt Cys	acc Thr	aca Thr	cat His 120	gtc Val	tac Tyr	ggt Gly	gcc Ala	ccc Pro 125	cgg Arg	aac Asn	tgg Trp	384
ggc Gly 130	cag Gln	gga Gly	tcc Ser	ctg Leu	gtc Val 135	acc Thr	gtc Val	tcc Ser	tca Ser	gcc Ala	tcc Ser 140	acc Thr	aag Lys	ggc Gly	cca Pro	432
aag Lys 145	ctt Leu	gaa Glu	gaa Glu	ggt Gly	gaa Glu 150	ttt Phe	tca Ser	gaa Glu	gca Ala	cgc Arg 155	gta Val	cag Gln	tct Ser	gtg Val	ttg Leu 160	480
act Thr	cag Gln	ccg Pro	ccc Pro	tca Ser 165	gtg Val	tct Ser	gcg Ala	gcc Ala	cca Pro 170	gga Gly	cag Gln	aag Lys	gtc Val 175	acc Thr	atc Ile	528
tcc Ser	tgc Cys	tct Ser	gga Gly 180	agc Ser	agc Ser	tcc Ser	aac Asn	att Ile 185	gga Gly	aat Asn	aat Asn	tat Tyr	gtc Val 190	tcc Ser	tgg Trp	576
tac Tyr	gtt Val	caa Gln 195	ctc Leu	cca Pro	gga Gly	aca Thr	gcc Ala 200	ccc Pro	aaa Lys	ctc Leu	ctc Leu	att Ile 205	tat Tyr	gac Asp	aat Asn	624
aat Asn 210	aag Lys	cga Arg	ttc Phe	tca Ser	gga Gly	gtt Val 215	cct Pro	gac Asp	cga Arg	ttc Phe	tct Ser 220	ggc Gly	tcc Ser	aag Lys	tct Ser	672
ggc Gly 225	acg Thr	tca Ser	gcc Ala	acc Thr	ctg Leu 230	ggc Gly	atc Ile	acc Thr	ggg Gly	ctc Leu 235	cag Gln	act Thr	ggg Gly	gac Asp	gag Glu 240	720
gcc Ala	gat Asp	tat Tyr	tac Tyr	tgc Cys 245	gga Gly	gca Ala	tgg Trp	gat Asp	ggc Gly 250	agc Ser	ctg Leu	cgt Arg	gaa Glu	gcg Ala 255	gta Val	768
ttc Phe	ggc Gly	gga Gly	ggg Gly 260	acc Thr	aag Lys	gtc Val	acc Thr	gtc Val 265	cta Leu	ggt Gly	gcg Ala	gcc Ala	gca Ala 270	gtt Val	gag Glu	816
ctc Leu	gag Glu	gcg Ala 275	gcc Ala	gcg Ala	gat Asp	tac Tyr	aaa Lys 280	gac Asp	gat Asp	gac Asp	gat Asp	aaa Lys 285	gaa Glu	ttc Phe	acg Thr	864
cgt Arg 290	gaa Glu	aaa Lys	aag Lys	gag Glu	ctg Leu	agg Arg 295	aaa Lys	gtg Val	gcc Ala	cat His	tta Leu 300	aca Thr	ggc Gly	aag Lys	tcc Ser	912

TherapheresisSeq Listing.txt

aac tca agg tcc atg cct ctg gaa tgg gaa gac acc tat gga att gtc Asn Ser Arg Ser Met Pro Leu Glu Trp Glu Asp Thr Tyr Gly Ile Val 305 310 315 320	960
ctg ctt tct gga gtg aag tat aag aag ggt ggc ctt gtg atc aat gaa Leu Leu Ser Gly Val Lys Tyr Lys Lys Gly Gly Leu Val Ile Asn Glu 325 330 335	1008
act ggg ctg tac ttt gta tat tcc aaa gta tac ttc cgg ggt caa tct Thr Gly Leu Tyr Phe Val Tyr Ser Lys Val Tyr Phe Arg Gly Gln Ser 340 345 350	1056
tgc aac aac ctg ccc ctg agc cac aag gtc tac atg agg aac tct aag Cys Asn Asn Leu Pro Leu Ser His Lys Val Tyr Met Arg Asn Ser Lys 355 360 365	1104
tat ccc cag gat ctg gtg atg atg gag ggg aag atg atg agc tac tgc Tyr Pro Gln Asp Leu Val Met Met Glu Gly Lys Met Met Ser Tyr Cys 370 375 380	1152
act act ggg cag atg tgg gcc cgc agc agc tac ctg ggg gca gtg ttc Thr Thr Gly Gln Met Trp Ala Arg Ser Ser Tyr Leu Gly Ala Val Phe 385 390 395 400	1200
aat ctt acc agt gct gat cat tta tat gtc aac gta tct gag ctc tct Asn Leu Thr Ser Ala Asp His Leu Tyr Val Asn Val Ser Glu Leu Ser 405 410 415	1248
ctg gtc aat ttt gag gaa tct cag acg ttt ttc ggc tta tat aag ctc Leu Val Asn Phe Glu Glu Ser Gln Thr Phe Phe Gly Leu Tyr Lys Leu 420 425 430	1296
ggt ggc ggt tct ggt ggc ggt tct ggt ggc ggt tct ggt ggc gga tca Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser 435 440 445	1344
gaa aaa aag gag ctg agg aaa gtg gcc cat tta aca ggc aag tcc aac Glu Lys Lys Glu Leu Arg Lys Val Ala His Leu Thr Gly Lys Ser Asn 450 455 460	1392
tca agg tcc atg cct ctg gaa tgg gaa gac acc tat gga att gtc ctg Ser Arg Ser Met Pro Leu Glu Trp Glu Asp Thr Tyr Gly Ile Val Leu 465 470 475 480	1440
ctt tct gga gtg aag tat aag aag ggt ggc ctt gtg atc aat gaa act Leu Ser Gly Val Lys Tyr Lys Lys Gly Gly Leu Val Ile Asn Glu Thr 485 490 495	1488
ggg ctg tac ttt gta tat tcc aaa gta tac ttc cgg ggt caa tct tgc Gly Leu Tyr Phe Val Tyr Ser Lys Val Tyr Phe Arg Gly Gln Ser Cys 500 505 510	1536
aac aac ctg ccc ctg agc cac aag gtc tac atg agg aac tct aag tat Asn Asn Leu Pro Leu Ser His Lys Val Tyr Met Arg Asn Ser Lys Tyr 515 520 525	1584
ccc cag gat ctg gtg atg atg gag ggg aag atg atg agc tac tgc act Pro Gln Asp Leu Val Met Met Glu Gly Lys Met Met Ser Tyr Cys Thr 530 535 540	1632
act ggg cag atg tgg gcc cgc agc agc tac ctg ggg gca gtg ttc aat Thr Gly Gln Met Trp Ala Arg Ser Ser Tyr Leu Gly Ala Val Phe Asn 545 550 555 560	1680

TherapheresisSeq Listing.txt

ctt acc agt gct gat cat tta tat gtc aac gta tct gag ctc tct ctg	1728
Leu Thr Ser Ala Asp His Leu Tyr Val Asn Val Ser Glu Leu Ser Leu	
565 570 575	
gtc aat ttt gag gaa tct cag acg ttt ttc ggc tta tat aag ctc ggt	1776
Val Asn Phe Glu Glu Ser Gln Thr Phe Phe Gly Leu Tyr Lys Leu Gly	
580 585 590	
ggc ggt tct ggt ggc ggt tct ggt ggc ggt tct ggt ggc gga tcc gaa	1824
Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu	
595 600 605	
aaa aag gag ctg agg aaa gtg gcc cat tta aca ggc aag tcc aac tca	1872
Lys Lys Glu Leu Arg Lys Val Ala His Leu Thr Gly Lys Ser Asn Ser	
610 615 620	
agg tcc atg cct ctg gaa tgg gaa gac acc tat gga att gtc ctg ctt	1920
Arg Ser Met Pro Leu Glu Trp Glu Asp Thr Tyr Gly Ile Val Leu Leu	
625 630 635 640	
tct gga gtg aag tat aag aag ggt ggc ctt gtg atc aat gaa act ggg	1968
Ser Gly Val Lys Tyr Lys Lys Gly Gly Leu Val Ile Asn Glu Thr Gly	
645 650 655	
ctg tac ttt gta tat tcc aaa gta tac ttc cgg ggt caa tct tgc aac	2016
Leu Tyr Phe Val Tyr Ser Lys Val Tyr Phe Arg Gly Gln Ser Cys Asn	
660 665 670	
aac ctg ccc ctg agc cac aag gtc tac atg agg aac tct aag tat ccc	2064
Asn Leu Pro Leu Ser His Lys Val Tyr Met Arg Asn Ser Lys Tyr Pro	
675 680 685	
cag gat ctg gtg atg atg gag ggg aag atg atg agc tac tgc act act	2112
Gln Asp Leu Val Met Met Glu Gly Lys Met Met Ser Tyr Cys Thr Thr	
690 695 700	
ggg cag atg tgg gcc cgc agc agc tac ctg ggg gca gtg ttc aat ctt	2160
Gly Gln Met Trp Ala Arg Ser Ser Tyr Leu Gly Ala Val Phe Asn Leu	
705 710 715 720	
acc agt gct gat cat tta tat gtc aac gta tct gag ctc tct ctg gtc	2208
Thr Ser Ala Asp His Leu Tyr Val Asn Val Ser Glu Leu Ser Leu Val	
725 730 735	
aat ttt gag gaa tct cag acg ttt ttc ggc tta tat aag ctc tga	2253
Asn Phe Glu Glu Ser Gln Thr Phe Phe Gly Leu Tyr Lys Leu	
740 745 750	

<210> 36

<211> 750

<212> PRT

<213> Artificial sequence

<220>

<223> Description of Artificial Sequence: scFasL-AMAIze peptide sequence

<400> 36

Met Asp Trp Thr Trp Arg Val Phe Cys Leu Leu Ala Val Ala Pro Gly
1 5 10 15

TherapheresisSeq Listing.txt

Ala His Ser Gln val Gln Leu val Gln Ser Gly Gly Gly Met val Glu
20 25 30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35 40 45

Ser Asn Ala Trp Met Ser Trp val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

Glu Trp val Gly Arg Ile Lys Ser Lys Ala Gly Gly Gly Thr Ala Glu
65 70 75 80

Tyr Ala Ala Pro val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser
85 90 95

Gln Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Asp Asp Thr
100 105 110

Ala val Tyr Tyr Cys Thr Thr His val Tyr Gly Ala Pro Arg Asn Trp
115 120 125

Gly Gln Gly Ser Leu val Thr val Ser Ser Ala Ser Thr Lys Gly Pro
130 135 140

Lys Leu Glu Glu Gly Glu Phe Ser Glu Ala Arg val Gln Ser val Leu
145 150 155 160

Thr Gln Pro Pro Ser val Ser Ala Ala Pro Gly Gln Lys val Thr Ile
165 170 175

Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn Tyr val Ser Trp
180 185 190

Tyr val Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Asp Asn
195 200 205

Asn Lys Arg Phe Ser Gly val Pro Asp Arg Phe Ser Gly Ser Lys Ser
210 215 220

Gly Thr Ser Ala Thr Leu Gly Ile Thr Gly Leu Gln Thr Gly Asp Glu
225 230 235 240

Ala Asp Tyr Tyr Cys Gly Ala Trp Asp Gly Ser Leu Arg Glu Ala val
245 250 255

Phe Gly Gly Gly Thr Lys val Thr val Leu Gly Ala Ala Ala val Glu
260 265 270

TherapheresisSeq Listing.txt

Leu Glu Ala Ala Ala Asp Tyr Lys Asp Asp Asp Asp Lys Glu Phe Thr
275 280 285

Arg Glu Lys Lys Glu Leu Arg Lys Val Ala His Leu Thr Gly Lys Ser
290 295 300

Asn Ser Arg Ser Met Pro Leu Glu Trp Glu Asp Thr Tyr Gly Ile Val
305 310 315 320

Leu Leu Ser Gly Val Lys Tyr Lys Lys Gly Gly Leu Val Ile Asn Glu
325 330 335

Thr Gly Leu Tyr Phe Val Tyr Ser Lys Val Tyr Phe Arg Gly Gln Ser
340 345 350

Cys Asn Asn Leu Pro Leu Ser His Lys Val Tyr Met Arg Asn Ser Lys
355 360 365

Tyr Pro Gln Asp Leu Val Met Met Glu Gly Lys Met Met Ser Tyr Cys
370 375 380

Thr Thr Gly Gln Met Trp Ala Arg Ser Ser Tyr Leu Gly Ala Val Phe
385 390 395 400

Asn Leu Thr Ser Ala Asp His Leu Tyr Val Asn Val Ser Glu Leu Ser
405 410 415

Leu Val Asn Phe Glu Glu Ser Gln Thr Phe Phe Gly Leu Tyr Lys Leu
420 425 430

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
435 440 445

Glu Lys Lys Glu Leu Arg Lys Val Ala His Leu Thr Gly Lys Ser Asn
450 455 460

Ser Arg Ser Met Pro Leu Glu Trp Glu Asp Thr Tyr Gly Ile Val Leu
465 470 475 480

Leu Ser Gly Val Lys Tyr Lys Lys Gly Gly Leu Val Ile Asn Glu Thr
485 490 495

Gly Leu Tyr Phe Val Tyr Ser Lys Val Tyr Phe Arg Gly Gln Ser Cys
500 505 510

Asn Asn Leu Pro Leu Ser His Lys Val Tyr Met Arg Asn Ser Lys Tyr
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TherapheresisSeq Listing.txt

515

520

525

Pro Gln Asp Leu Val Met Met Glu Gly Lys Met Met Ser Tyr Cys Thr
530 535 540

Thr Gly Gln Met Trp Ala Arg Ser Ser Tyr Leu Gly Ala Val Phe Asn
545 550 555 560

Leu Thr Ser Ala Asp His Leu Tyr Val Asn Val Ser Glu Leu Ser Leu
565 570 575

Val Asn Phe Glu Glu Ser Gln Thr Phe Phe Gly Leu Tyr Lys Leu Gly
580 585 590

Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu
595 600 605

Lys Lys Glu Leu Arg Lys Val Ala His Leu Thr Gly Lys Ser Asn Ser
610 615 620

Arg Ser Met Pro Leu Glu Trp Glu Asp Thr Tyr Gly Ile Val Leu Leu
625 630 635 640

Ser Gly Val Lys Tyr Lys Lys Gly Gly Leu Val Ile Asn Glu Thr Gly
645 650 655

Leu Tyr Phe Val Tyr Ser Lys Val Tyr Phe Arg Gly Gln Ser Cys Asn
660 665 670

Asn Leu Pro Leu Ser His Lys Val Tyr Met Arg Asn Ser Lys Tyr Pro
675 680 685

Gln Asp Leu Val Met Met Glu Gly Lys Met Met Ser Tyr Cys Thr Thr
690 695 700

Gly Gln Met Trp Ala Arg Ser Ser Tyr Leu Gly Ala Val Phe Asn Leu
705 710 715 720

Thr Ser Ala Asp His Leu Tyr Val Asn Val Ser Glu Leu Ser Leu Val
725 730 735

Asn Phe Glu Glu Ser Gln Thr Phe Phe Gly Leu Tyr Lys Leu
740 745 750

<210> 37
<211> 2646
<212> DNA
<213> Artificial sequence

TherapheresisSeq Listing.txt

<220>

<223> Description of Artificial Sequence: scTRAIL-AMAIze sequence

<220>

<221> CDS

<222> (1)..(2643)

<400> 37

atg gac tgg acc tgg cgc gtg ttt tgc ctg ctc gcc gtg gct cct ggg	48
Met Asp Trp Thr Trp Arg Val Phe Cys Leu Leu Ala Val Ala Pro Gly	
1 5 10 15	

gcc cac agc cag gta cag ctg gtg cag tct ggg gga ggc atg gta gag	96
Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Gly Gly Met Val Glu	
20 25 30	

cct ggg ggg tcc ctt aga ctc tcc tgt gca gcc tct gga ttc act ttc	144
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe	
35 40 45	

agt aat gcc tgg atg agc tgg gtc cgc cag gct cca ggg aag ggg ctg	192
Ser Asn Ala Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu	
50 55 60	

gag tgg gtt ggc cgt ata aaa agc aaa gct ggt ggt ggg aca gca gag	240
Glu Trp Val Gly Arg Ile Lys Ser Lys Ala Gly Gly Gly Thr Ala Glu	
65 70 75 80	

tac gct gca ccc gtg aaa ggc aga ttc acc atc tca aga gat gat tca	288
Tyr Ala Ala Pro Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser	
85 90 95	

caa aac acg ctg tat ctg caa atg aac agc ctg aaa acc gac gac aca	336
Gln Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Asp Asp Thr	
100 105 110	

gcc gtg tat tac tgt acc aca cat gtc tac ggt gcc ccc cgg aac tgg	384
Ala Val Tyr Tyr Cys Thr Thr His Val Tyr Gly Ala Pro Arg Asn Trp	
115 120 125	

ggc cag gga tcc ctg gtc acc gtc tcc tca gcc tcc acc aag ggc cca	432
Gly Gln Gly Ser Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro	
130 135 140	

aag ctt gaa gaa ggt gaa ttt tca gaa gca cgc gta cag tct gtg ttg	480
Lys Leu Glu Glu Gly Glu Phe Ser Glu Ala Arg Val Gln Ser Val Leu	
145 150 155 160	

act cag ccg ccc tca gtg tct gcg gcc cca gga cag aag gtc acc atc	528
Thr Gln Pro Pro Ser Val Ser Ala Ala Pro Gly Gln Lys Val Thr Ile	
165 170 175	

tcc tgc tct gga agc agc tcc aac att gga aat aat tat gtc tcc tgg	576
Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn Tyr Val Ser Trp	
180 185 190	

tac gtt caa ctc cca gga aca gcc ccc aaa ctc ctc att tat gac aat	624
Tyr Val Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Asp Asn	
195 200 205	

TherapheresisSeq Listing.txt

aat aag cga ttc tca gga gtt cct gac cga ttc tct ggc tcc aag tct Asn Lys Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser 210 215 220	672
ggc acg tca gcc acc ctg ggc atc acc ggg ctc cag act ggg gac gag Gly Thr Ser Ala Thr Leu Gly Ile Thr Gly Leu Gln Thr Gly Asp Glu 225 230 235 240	720
gcc gat tat tac tgc gga gca tgg gat ggc agc ctg cgt gaa gcg gta Ala Asp Tyr Tyr Cys Gly Ala Trp Asp Gly Ser Leu Arg Glu Ala Val 245 250 255	768
ttc ggc gga ggg acc aag gtc acc gtc cta ggt gcg gcc gca gtt gag Phe Gly Gly Gly Thr Lys Val Thr Val Leu Gly Ala Ala Ala Val Glu 260 265 270	816
ctc gag gcg gcc gcg gat tac aaa gac gat gac gat aaa gaa ttc gga Leu Glu Ala Ala Ala Asp Tyr Lys Asp Asp Asp Lys Glu Phe Gly 275 280 285	864
acc tct gag gaa acc att tct aca gtt caa gaa aag caa caa aat att Thr Ser Glu Glu Thr Ile Ser Thr Val Gln Glu Lys Gln Gln Asn Ile 290 295 300	912
tct ccc cta gtg aga gaa aga ggt cct cag aga gta gca gct cac ata Ser Pro Leu Val Arg Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile 305 310 315 320	960
act ggg acc aga gga aga agc aac aca ttg tct tct cca aac tcc aag Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys 325 330 335	1008
aat gaa aag gct ctg ggc cgc aaa ata aac tcc tgg gaa tca tca agg Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg 340 345 350	1056
agt ggg cat tca ttc ctg agc aac ttg cac ttg agg aat ggt gaa ctg Ser Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu 355 360 365	1104
gtc atc cat gaa aaa ggg ttt tac tac atc tat tcc caa aca tac ttt Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe 370 375 380	1152
cga ttt cag gag gaa ata aaa gaa aac aca aag aac gac aaa caa atg Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met 385 390 395 400	1200
gtc caa tat att tac aaa tac aca agt tat cct gac cct ata ttg ttg Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu 405 410 415	1248
atg aaa agt gct aga aat agt tgt tgg tct aaa gat gca gaa tat gga Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly 420 425 430	1296
ctc tat tcc atc tat caa ggg gga ata ttt gag ctt aag gaa aat gac Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp 435 440 445	1344

TherapheresisSeq Listing.txt

aga att ttt gtt tct gta aca aat gag cac ttg ata gac atg gac cat Arg Ile Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His 450 455 460	1392
gaa gcc agt ttt ttc ggg gcc ttt tta gtt ggc ggt ggc ggt tct ggt Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly Gly Gly Ser Gly 465 470 475 480	1440
ggc ggt tct ggt ggc ggt tct ggt ggc gga tca acc tct gag gaa acc Gly Gly Ser Gly Gly Ser Ser Gly Ser Thr Ser Glu Glu Thr 485 490 495	1488
att tct aca gtt caa gaa aag caa caa aat att tct ccc cta gtg aga Ile Ser Thr Val Gln Glu Lys Gln Gln Asn Ile Ser Pro Leu Val Arg 500 505 510	1536
gaa aga ggt cct cag aga gta gca gct cac ata act ggg acc aga gga Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly 515 520 525	1584
aga agc aac aca ttg tct tct cca aac tcc aag aat gaa aag gct ctg Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu 530 535 540	1632
ggc cgc aaa ata aac tcc tgg gaa tca tca agg agt ggg cat tca ttc Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe 545 550 555 560	1680
ctg agc aac ttg cac ttg agg aat ggt gaa ctg gtc atc cat gaa aaa Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys 565 570 575	1728
ggg ttt tac tac atc tat tcc caa aca tac ttt cga ttt cag gag gaa Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu 580 585 590	1776
ata aaa gaa aac aca aag aac gac aaa caa atg gtc caa tat att tac Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr 595 600 605	1824
aaa tac aca agt tat cct gac cct ata ttg ttg atg aaa agt gct aga Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg 610 615 620	1872
aat agt tgt tgg tct aaa gat gca gaa tat gga ctc tat tcc atc tat Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr 625 630 635 640	1920
caa ggg gga ata ttt gag ctt aag gaa aat gac aga att ttt gtt tct Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser 645 650 655	1968
gta aca aat gag cac ttg ata gac atg gac cat gaa gcc agt ttt ttc Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe 660 665 670	2016
ggg gcc ttt tta gtt ggc ggt ggc ggt tct ggt ggc ggt tct ggt ggc Gly Ala Phe Leu Val Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly 675 680 685	2064
ggt tct ggt ggc gga tcc acc tct gag gaa acc att tct aca gtt caa	2112

TherapheresisSeq Listing.txt

Gly 690	Ser	Gly	Gly	Gly	Ser	Thr 695	Ser	Glu	Glu	Thr	Ile 700	Ser	Thr	Val	Gln	
gaa Glu 705	aag Lys	caa Gln	caa Gln	aat Asn	att Ile 710	tct Ser	ccc Pro	cta Leu	gtg Val	aga Arg 715	gaa Glu	aga Arg	ggt Gly	cct Pro	cag Gln 720	2160
aga Arg	gta Val	gca Ala	gct Ala	cac His 725	ata Ile	act Thr	ggg Gly	acc Thr	aga Arg 730	gga Gly	aga Arg	agc Ser	aac Asn	aca Thr 735	ttg Leu	2208
tct Ser	tct Ser	cca Pro	aac Asn 740	tcc Ser	aag Lys	aat Asn	gaa Glu	aag Lys 745	gct Ala	ctg Leu	ggc Gly	cgc Arg	aaa Lys 750	ata Ile	aac Asn	2256
tcc Ser	tgg Trp	gaa Glu 755	tca Ser	tca Ser	agg Arg	agt Ser	ggg Gly 760	cat His	tca Ser	ttc Phe	ctg Leu	agc Ser 765	aac Asn	ttg Leu	cac His	2304
ttg Leu 770	agg Arg	aat Asn	ggt Gly	gaa Glu	ctg Leu 775	gtc Val	atc Ile	cat His	gaa Glu	aaa Lys	ggg Gly 780	ttt Phe	tac Tyr	tac Tyr	atc Ile	2352
tat Tyr 785	tcc Ser	caa Gln	aca Thr	tac Tyr	ttt Phe 790	cga Arg	ttt Phe	cag Gln	gag Glu	gaa Glu 795	ata Ile	aaa Lys	gaa Glu	aac Asn	aca Thr 800	2400
aag Lys	aac Asn	gac Asp	aaa Lys	caa Gln 805	atg Met	gtc Val	caa Gln	tat Tyr	att Ile 810	tac Tyr	aaa Lys	tac Tyr	aca Thr	agt Ser 815	tat Tyr	2448
cct Pro	gac Asp	cct Pro	ata Ile 820	ttg Leu	ttg Leu	atg Met	aaa Lys	agt Ser 825	gct Ala	aga Arg	aat Asn	agt Ser	tgt Cys 830	tgg Trp	tct Ser	2496
aaa Lys	gat Asp	gca Ala 835	gaa Glu	tat Tyr	gga Gly	ctc Leu	tat Tyr 840	tcc Ser	atc Ile	tat Tyr	caa Gln	ggg Gly 845	gga Gly	ata Ile	ttt Phe	2544
gag Glu 850	ctt Leu	aag Lys	gaa Glu	aat Asn	gac Asp	aga Arg 855	att Ile	ttt Phe	gtt Val	tct Ser	gta Val 860	aca Thr	aat Asn	gag Glu	cac His	2592
ttg Leu 865	ata Ile	gac Asp	atg Met	gac Asp	cat His 870	gaa Glu	gcc Ala	agt Ser	ttt Phe	ttc Phe 875	ggg Gly	gcc Ala	ttt Phe	tta Leu	gtt Val 880	2640
ggc Gly	tga															2646

<210> 38
 <211> 881
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: scTRAIL-AMAIze peptide sequence

<400> 38

TherapheresisSeq Listing.txt

Met Asp Trp Thr Trp Arg Val Phe Cys Leu Leu Ala Val Ala Pro Gly
1 5 10 15

Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Gly Gly Met Val Glu
20 25 30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35 40 45

Ser Asn Ala Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

Glu Trp Val Gly Arg Ile Lys Ser Lys Ala Gly Gly Gly Thr Ala Glu
65 70 75 80

Tyr Ala Ala Pro Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser
85 90 95

Gln Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Asp Asp Thr
100 105 110

Ala Val Tyr Tyr Cys Thr Thr His Val Tyr Gly Ala Pro Arg Asn Trp
115 120 125

Gly Gln Gly Ser Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
130 135 140

Lys Leu Glu Glu Gly Glu Phe Ser Glu Ala Arg Val Gln Ser Val Leu
145 150 155 160

Thr Gln Pro Pro Ser Val Ser Ala Ala Pro Gly Gln Lys Val Thr Ile
165 170 175

Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn Tyr Val Ser Trp
180 185 190

Tyr Val Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Asp Asn
195 200 205

Asn Lys Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser
210 215 220

Gly Thr Ser Ala Thr Leu Gly Ile Thr Gly Leu Gln Thr Gly Asp Glu
225 230 235 240

Ala Asp Tyr Tyr Cys Gly Ala Trp Asp Gly Ser Leu Arg Glu Ala Val
245 250 255

TherapheresisSeq Listing.txt

Phe Gly Gly Gly Thr Lys Val Thr Val Leu Gly Ala Ala Ala Val Glu
 260 265 270
 Leu Glu Ala Ala Ala Asp Tyr Lys Asp Asp Asp Asp Lys Glu Phe Gly
 275 280 285
 Thr Ser Glu Glu Thr Ile Ser Thr Val Gln Glu Lys Gln Gln Asn Ile
 290 295 300
 Ser Pro Leu Val Arg Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile
 305 310 315 320
 Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys
 325 330 335
 Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg
 340 345 350
 Ser Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu
 355 360 365
 Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe
 370 375 380
 Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met
 385 390 395 400
 Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu
 405 410 415
 Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly
 420 425 430
 Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp
 435 440 445
 Arg Ile Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His
 450 455 460
 Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly Gly Gly Gly Ser Gly
 465 470 475 480
 Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Thr Ser Glu Glu Thr
 485 490 495
 Ile Ser Thr Val Gln Glu Lys Gln Gln Asn Ile Ser Pro Leu Val Arg

TherapheresisSeq Listing.txt

500

505

510

Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly
515 520 525

Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu
530 535 540

Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe
545 550 555 560

Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys
565 570 575

Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu
580 585 590

Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr
595 600 605

Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg
610 615 620

Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr
625 630 635 640

Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser
645 650 655

Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe
660 665 670

Gly Ala Phe Leu Val Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
675 680 685

Gly Ser Gly Gly Gly Ser Thr Ser Glu Glu Thr Ile Ser Thr Val Gln
690 695 700

Glu Lys Gln Gln Asn Ile Ser Pro Leu Val Arg Glu Arg Gly Pro Gln
705 710 715 720

Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu
725 730 735

Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn
740 745 750

TherapheresisSeq Listing.txt

Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His
755 760 765

Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile
770 775 780

Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr
785 790 795 800

Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr
805 810 815

Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser
820 825 830

Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe
835 840 845

Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His
850 855 860

Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val
865 870 875 880

Gly

<210> 39
<211> 2358
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: sCTNF-AMAIZE sequence

<220>
<221> CDS
<222> (1)..(2355)

<400> 39
atg gac tgg acc tgg cgc gtg ttt tgc ctg ctc gcc gtg gct cct ggg 48
Met Asp Trp Thr Trp Arg Val Phe Cys Leu Leu Ala Val Ala Pro Gly
1 5 10 15

gcc cac agc cag gta cag ctg gtg cag tct ggg gga ggc atg gta gag 96
Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Gly Gly Met Val Glu
20 25 30

cct ggg ggg tcc ctt aga ctc tcc tgt gca gcc tct gga ttc act ttc 144
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35 40 45

TherapheresisSeq Listing.txt

agt Ser	aat Asn	gcc Ala	tgg Trp	atg Met	agc Ser	tgg Trp	gtc Val	cgc Arg	cag Gln	gct Ala	cca Pro	ggg Gly	aag Lys	ggg Gly	ctg Leu	192
50						55					60					
gag Glu	tgg Trp	gtt Val	ggc Gly	cgt Arg	ata Ile	aaa Lys	agc Ser	aaa Lys	gct Ala	ggt Gly	ggt Gly	ggg Gly	aca Thr	gca Ala	gag Glu	240
65					70					75					80	
tac Tyr	gct Ala	gca Ala	ccc Pro	gtg Val	aaa Lys	ggc Gly	aga Arg	ttc Phe	acc Thr	atc Ile	tca Ser	aga Arg	gat Asp	gat Asp	tca Ser	288
				85					90					95		
caa Gln	aac Asn	acg Thr	ctg Leu	tat Tyr	ctg Leu	caa Gln	atg Met	aac Asn	agc Ser	ctg Leu	aaa Lys	acc Thr	gac Asp	gac Asp	aca Thr	336
			100					105					110			
gcc Ala	gtg Val	tat Tyr	tac Tyr	tgt Cys	acc Thr	aca Thr	cat His	gtc Val	tac Tyr	ggt Gly	gcc Ala	ccc Pro	cgg Arg	aac Asn	tgg Trp	384
		115					120					125				
ggc Gly	cag Gln	gga Gly	tcc Ser	ctg Leu	gtc Val	acc Thr	gtc Val	tcc Ser	tca Ser	gcc Ala	tcc Ser	acc Thr	aag Lys	ggc Gly	cca Pro	432
	130					135					140					
aag Lys	ctt Leu	gaa Glu	gaa Glu	ggt Gly	gaa Glu	ttt Phe	tca Ser	gaa Glu	gca Ala	cgc Arg	gta Val	cag Gln	tct Ser	gtg Val	ttg Leu	480
	145			150						155					160	
act Thr	cag Gln	ccg Pro	ccc Pro	tca Ser	gtg Val	tct Ser	gcg Ala	gcc Ala	cca Pro	gga Gly	cag Gln	aag Lys	gtc Val	acc Thr	atc Ile	528
				165					170					175		
tcc Ser	tgc Cys	tct Ser	gga Gly	agc Ser	agc Ser	tcc Ser	aac Asn	att Ile	gga Gly	aat Asn	aat Asn	tat Tyr	gtc Val	tcc Ser	tgg Trp	576
			180					185					190			
tac Tyr	gtt Val	caa Gln	ctc Leu	cca Pro	gga Gly	aca Thr	gcc Ala	ccc Pro	aaa Lys	ctc Leu	ctc Leu	att Ile	tat Tyr	gac Asp	aat Asn	624
		195					200					205				
aat Asn	aag Lys	cga Arg	ttc Phe	tca Ser	gga Gly	gtt Val	cct Pro	gac Asp	cga Arg	ttc Phe	tct Ser	ggc Gly	tcc Ser	aag Lys	tct Ser	672
	210					215					220					
ggc Gly	acg Thr	tca Ser	gcc Ala	acc Thr	ctg Leu	ggc Gly	atc Ile	acc Thr	ggg Gly	ctc Leu	cag Gln	act Thr	ggg Gly	gac Asp	gag Glu	720
	225				230					235					240	
gcc Ala	gat Asp	tat Tyr	tac Tyr	tgc Cys	gga Gly	gca Ala	tgg Trp	gat Asp	ggc Gly	agc Ser	ctg Leu	cgt Arg	gaa Glu	gcg Ala	gta Val	768
				245					250					255		
ttc Phe	ggc Gly	gga Gly	ggg Gly	acc Thr	aag Lys	gtc Val	acc Thr	gtc Val	cta Leu	ggt Gly	gcg Ala	gcc Ala	gca Ala	gtt Val	gag Glu	816
			260					265					270			
ctc Leu	gag Glu	gcg Ala	gcc Ala	gcg Ala	gat Asp	tac Tyr	aaa Lys	gac Asp	gat Asp	gac Asp	gat Asp	aaa Lys	gaa Glu	ttc Phe	gga Gly	864
		275					280					285				
tca Ser	tct Ser	tct Ser	cga Arg	acc Thr	ccg Pro	agt Ser	gac Asp	aag Lys	cct Pro	gta Val	gcc Ala	cat His	gtt Val	gta Val	gca Ala	912
	290					295					300					

TherapheresisSeq Listing.txt

aac cct caa gct gag ggg cag ctc cag tgg ctg aac cgc cgg gcc aat Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn 305 310 315 320	960
gcc ctc ctg gcc aat ggc gtg gag ctg aga gat aac cag ctg gtg gtg Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val 325 330 335	1008
cca tca gag ggc ctg tac ctc atc tac tcc cag gtc ctc ttc aag ggc Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly 340 345 350	1056
caa ggc tgc ccc tcc acc cat gtg ctc ctc acc cac acc atc agc cgc Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile Ser Arg 355 360 365	1104
atc gcc gtc tcc tac cag acc aag gtc aac ctc ctc tct gcc atc aag Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys 370 375 380	1152
agc ccc tgc cag agg gag acc cca gag ggg gct gag gcc aag ccc tgg Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp 385 390 400	1200
tat gag ccc atc tat ctg gga ggc gtc ttc cag ctg gag aag ggt gac Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp 405 410 415	1248
cga ctc agc gct gag atc aat cgg ccc gac tat ctc gac ttt gcc gag Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu 420 425 430	1296
tct ggg cag gtc tac ttt ggg atc att gcc ctg ggt ggc ggt tct ggt Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu Gly Gly Gly Ser Gly 435 440 445	1344
ggc ggt tct ggt ggc ggt tct ggt ggc gga tca tca tct tct cga acc Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser Ser Ser Arg Thr 450 455 460	1392
ccg agt gac aag cct gta gcc cat gtt gta gca aac cct caa gct gag Pro Ser Asp Lys Pro Val Ala His Val Val Ala Asn Pro Gln Ala Glu 465 470 475 480	1440
ggg cag ctc cag tgg ctg aac cgc cgg gcc aat gcc ctc ctg gcc aat Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn 485 490 495	1488
ggc gtg gag ctg aga gat aac cag ctg gtg gtg cca tca gag ggc ctg Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser Glu Gly Leu 500 505 510	1536
tac ctc atc tac tcc cag gtc ctc ttc aag ggc caa ggc tgc ccc tcc Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser 515 520 525	1584
acc cat gtg ctc ctc acc cac acc atc agc cgc atc gcc gtc tcc tac Thr His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala Val Ser Tyr 530 535 540	1632
cag acc aag gtc aac ctc ctc tct gcc atc aag agc ccc tgc cag agg Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg 545	1680

TherapheresisSeq Listing.txt

545		550		555		560										
gag Glu	acc Thr	cca Pro	gag Glu	ggg Gly 565	gct Ala	gag Glu	gcc Ala	aag Lys	ccc Pro 570	tgg Trp	tat Tyr	gag Glu	ccc Pro	atc Ile 575	tat Tyr	1728
ctg Leu	gga Gly	ggg Gly	gtc Val 580	ttc Phe	cag Gln	ctg Leu	gag Glu	aag Lys 585	ggt Gly	gac Asp	cga Arg	ctc Leu	agc Ser 590	gct Ala	gag Glu	1776
atc Ile	aat Asn	cgg Arg 595	ccc Pro	gac Asp	tat Tyr	ctc Leu	gac Asp 600	ttt Phe	gcc Ala	gag Glu	tct Ser	ggg Gly 605	cag Gln	gtc Val	tac Tyr	1824
ttt Phe	ggg Gly 610	atc Ile	att Ile	gcc Ala	ctg Leu	ggt Gly 615	ggc Gly	ggt Gly	tct Ser	ggt Gly	ggc Gly 620	ggt Gly	tct Ser	ggt Gly	ggc Gly	1872
ggt Gly 625	tct Ser	ggt Gly	ggc Gly	gga Gly	tca Ser 630	tca Ser	tct Ser	tct Ser	cga Arg	acc Thr 635	ccg Pro	agt Ser	gac Asp	aag Lys	cct Pro 640	1920
gta Val	gcc Ala	cat His	gtt Val 645	gta Val	gca Ala	aac Asn	cct Pro	caa Gln	gct Ala 650	gag Glu	ggg Gly	cag Gln	ctc Leu	cag Gln 655	tgg Trp	1968
ctg Leu	aac Asn	cgc Arg	cgg Arg 660	gcc Ala	aat Asn	gcc Ala	ctc Leu	ctg Leu 665	gcc Ala	aat Asn	ggc Gly	gtg Val	gag Glu 670	ctg Leu	aga Arg	2016
gat Asp	aac Asn	cag Gln 675	ctg Leu	gtg Val	gtg Val	cca Pro	tca Ser 680	gag Glu	ggc Gly	ctg Leu	tac Tyr	ctc Leu 685	atc Ile	tac Tyr	tcc Ser	2064
cag Gln 690	gtc Val	ctc Leu	ttc Phe	aag Lys	ggc Gly	caa Gln 695	ggc Gly	tgc Cys	ccc Pro	tcc Ser	acc Thr 700	cat His	gtg Val	ctc Leu	ctc Leu	2112
acc Thr 705	cac His	acc Thr	atc Ile	agc Ser	cgc Arg 710	atc Ile	gcc Ala	gtc Val	tcc Ser 715	tac Tyr	cag Gln	acc Thr	aag Lys	gtc Val 720	aac Asn	2160
ctc Leu	ctc Leu	tct Ser	gcc Ala 725	atc Ile	aag Lys	agc Ser	ccc Pro	tgc Cys	cag Gln 730	agg Arg	gag Glu	acc Thr	cca Pro	gag Glu 735	ggg Gly	2208
gct Ala	gag Glu	gcc Ala	aag Lys 740	ccc Pro	tgg Trp	tat Tyr	gag Glu	ccc Pro 745	atc Ile	tat Tyr	ctg Leu	gga Gly	ggg Gly 750	gtc Val	ttc Phe	2256
cag Gln	ctg Leu	gag Glu 755	aag Lys	ggt Gly	gac Asp	cga Arg	ctc Leu 760	agc Ser	gct Ala	gag Glu	atc Ile	aat Asn 765	cgg Arg	ccc Pro	gac Asp	2304
tat Tyr 770	ctc Leu	gac Asp	ttt Phe	gcc Ala	gag Glu	tct Ser 775	ggg Gly	cag Gln	gtc Val	tac Tyr	ttt Phe 780	ggg Gly	atc Ile	att Ile	gcc Ala	2352
ctg Leu 785	tga															2358

TherapheresisSeq Listing.txt

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<210> 40
<211> 785
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: TNF-AMAIze peptide sequence

<400> 40
Met Asp Trp Thr Trp Arg Val Phe Cys Leu Leu Ala Val Ala Pro Gly
1          5          10          15

Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Gly Gly Met Val Glu
20          25          30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35          40          45

Ser Asn Ala Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50          55          60

Glu Trp Val Gly Arg Ile Lys Ser Lys Ala Gly Gly Gly Thr Ala Glu
65          70          75          80

Tyr Ala Ala Pro Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser
85          90          95

Gln Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Asp Asp Thr
100         105         110

Ala Val Tyr Tyr Cys Thr Thr His Val Tyr Gly Ala Pro Arg Asn Trp
115         120         125

Gly Gln Gly Ser Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
130         135         140

Lys Leu Glu Glu Gly Glu Phe Ser Glu Ala Arg Val Gln Ser Val Leu
145         150         155         160

Thr Gln Pro Pro Ser Val Ser Ala Ala Pro Gly Gln Lys Val Thr Ile
165         170         175

Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn Tyr Val Ser Trp
180         185         190

Tyr Val Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Asp Asn
195         200         205

Asn Lys Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser

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TherapheresisSeq_Listing.txt

210
 215
 220
 Gly Thr Ser Ala Thr Leu Gly Ile Thr Gly Leu Gln Thr Gly Asp Glu
 225 230 235 240
 Ala Asp Tyr Tyr Cys Gly Ala Trp Asp Gly Ser Leu Arg Glu Ala Val
 245 250 255
 Phe Gly Gly Gly Thr Lys Val Thr Val Leu Gly Ala Ala Ala Val Glu
 260 265 270
 Leu Glu Ala Ala Ala Asp Tyr Lys Asp Asp Asp Asp Lys Glu Phe Gly
 275 280 285
 Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val Val Ala
 290 295 300
 Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn
 305 310 315 320
 Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val
 325 330 335
 Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly
 340 345 350
 Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile Ser Arg
 355 360 365
 Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys
 370 375 380
 Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp
 385 390 395 400
 Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp
 405 410 415
 Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu
 420 425 430
 Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu Gly Gly Gly Ser Gly
 435 440 445
 Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser Ser Ser Arg Thr
 450 455 460

TherapheresisSeq Listing.txt

Pro Ser Asp Lys Pro Val Ala His Val Val Ala Asn Pro Gln Ala Glu
465 470 475 480

Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn
485 490 495

Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser Glu Gly Leu
500 505 510

Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser
515 520 525

Thr His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala Val Ser Tyr
530 535 540

Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg
545 550 555 560

Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr
565 570 575

Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu
580 585 590

Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr
595 600 605

Phe Gly Ile Ile Ala Leu Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
610 615 620

Gly Ser Gly Gly Gly Ser Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro
625 630 635 640

Val Ala His Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp
645 650 655

Leu Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg
660 665 670

Asp Asn Gln Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser
675 680 685

Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu
690 695 700

Thr His Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn
705 710 715 720

TherapheresisSeq Listing.txt

Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly
725 730 735

Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe
740 745 750

Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp
755 760 765

Tyr Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala
770 775 780

Leu
785

<210> 41

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Peptide linker sequence

<400> 41

Gly Gly Gly Ser

1